

**This Page Is Inserted by IFW Operations  
and is not a part of the Official Record**

## **BEST AVAILABLE IMAGES**

**Defective images within this document are accurate representations of the original documents submitted by the applicant.**

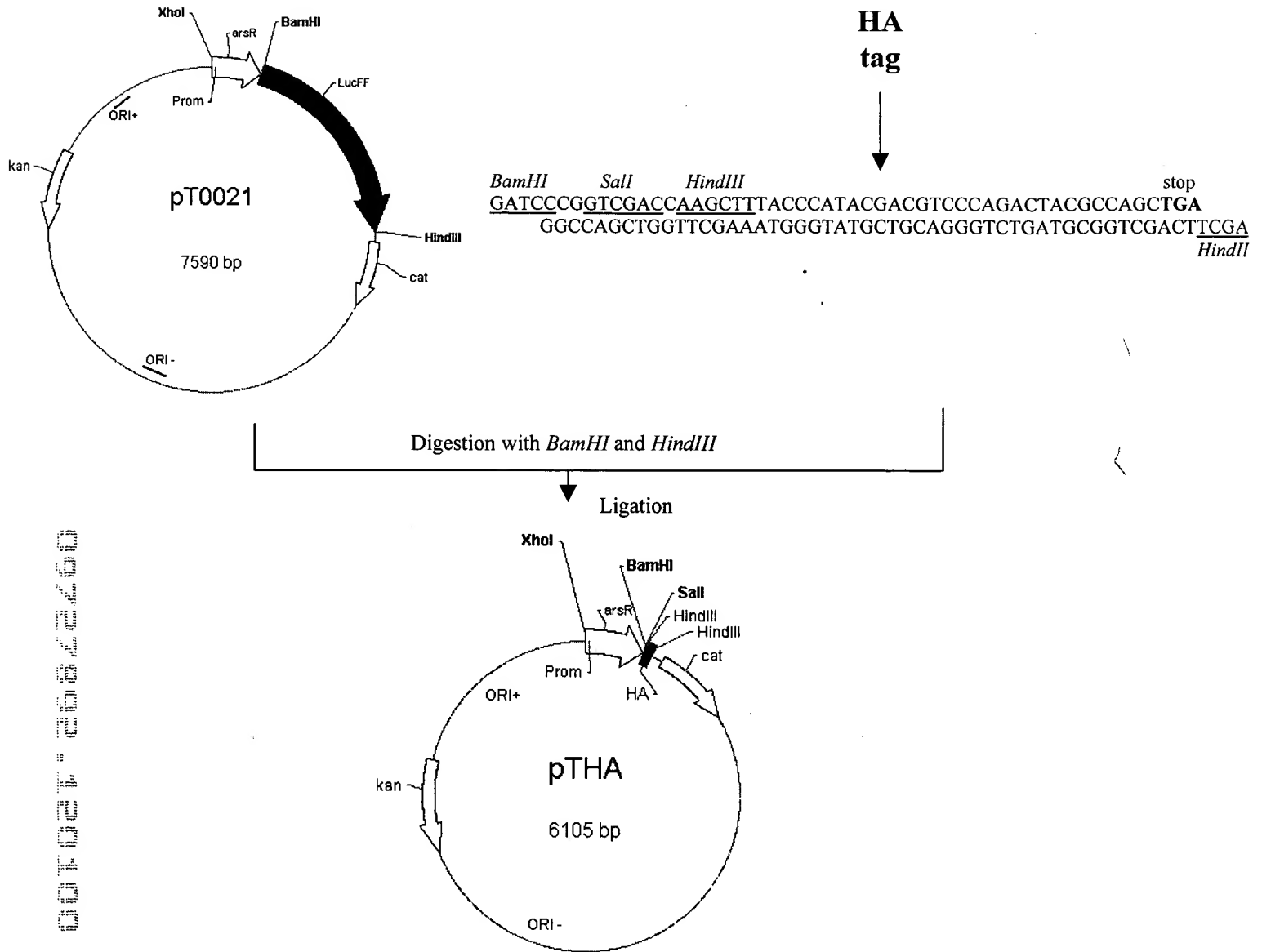
**Defects in the images may include (but are not limited to):**

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

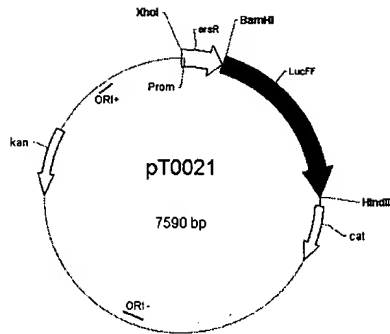
FIGURE 1A



B-

FIGURE 1B

PCR of pT0021 with XhoF and BamHNR



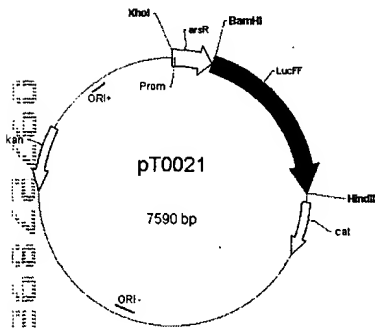
XhoF-5'-AATTCTCGAGTAAAATAACAT-3  
*XhoI*

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR  
Stop of *arsR* RBS *BamHI*

Digestion with *XhoI* and *BamHI*

Ligation

PCR of pT0021 with LucFFB and LucFFH



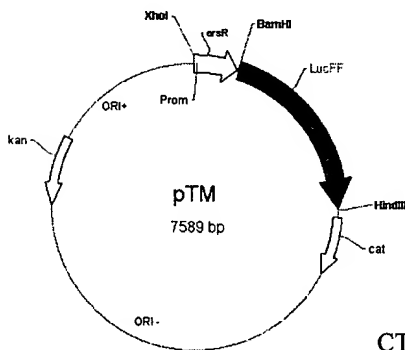
LucFFB-5'-CGGGATCCATGAGGGGTTCGAAGACG  
*BamHI* Start of LucFF Original *BamHI* was modified

GAAAGTCCAAATTGTAAGCTTGGG-LucFFH  
Stop of *HindIII* LucFF

Modified between stop of *arsR* to *BamHI*

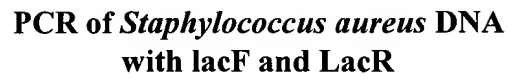
Digestion with *BamHI* and *HindIII*

Ligation



- Modified in the vicinity of *BamHI*
- Cloning site for ORFs: *BamHI* and *HindIII*
- No additional codons in the induced protein

CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT  
*XhoI* Prom *arsR* RBS *BamHI* LucFF *HindIII*

[illegible]

GTAAAAGGAGTCTTATTGGATCCCG-LacR  
*Bam*HI

## Ligation

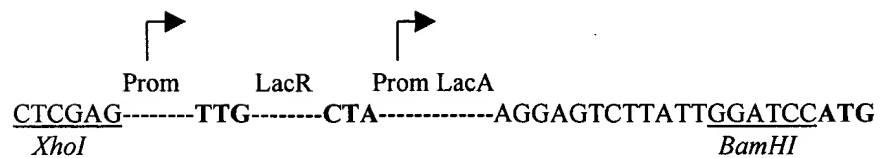


FIGURE 2A

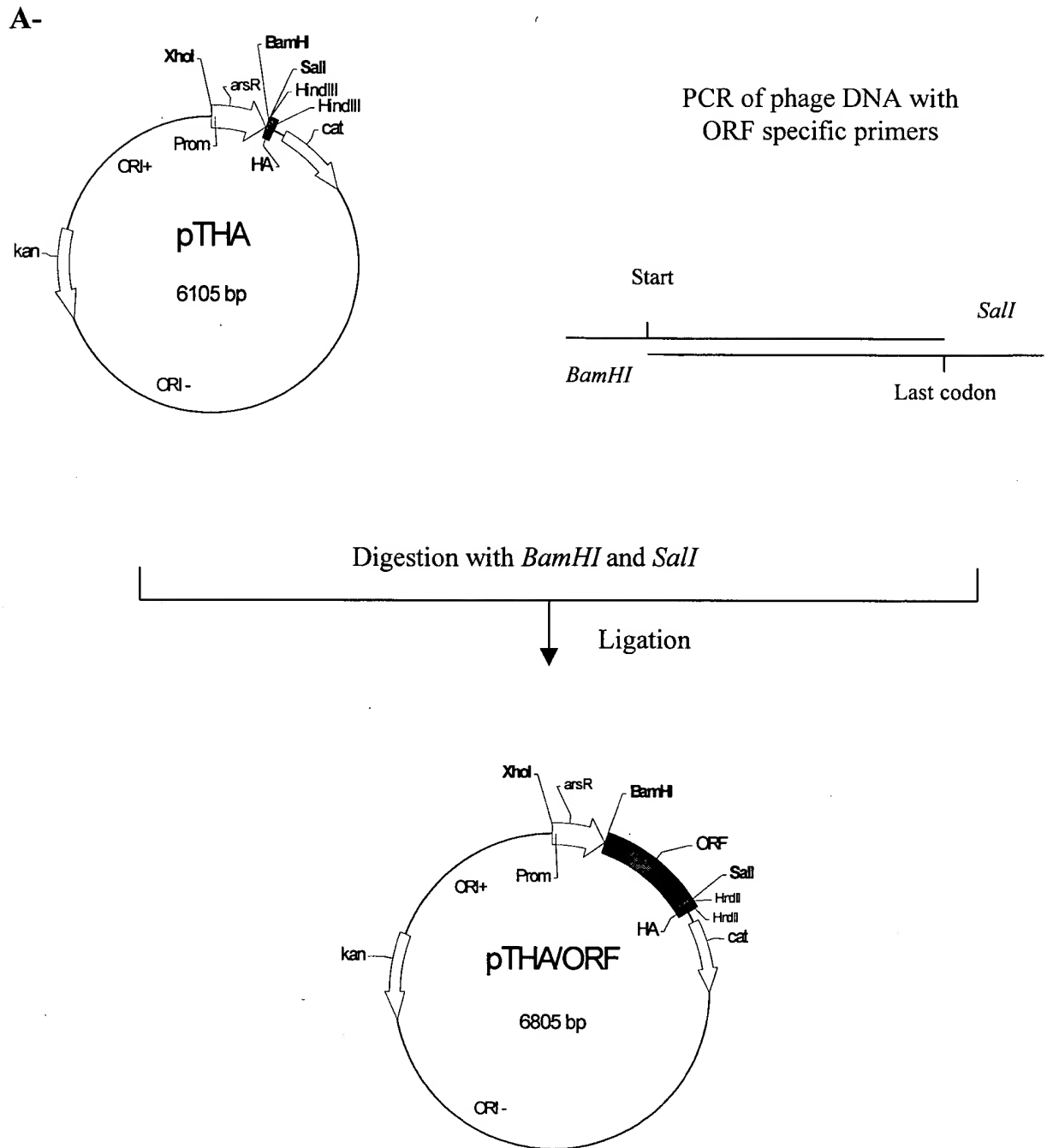


FIGURE 2B

B-

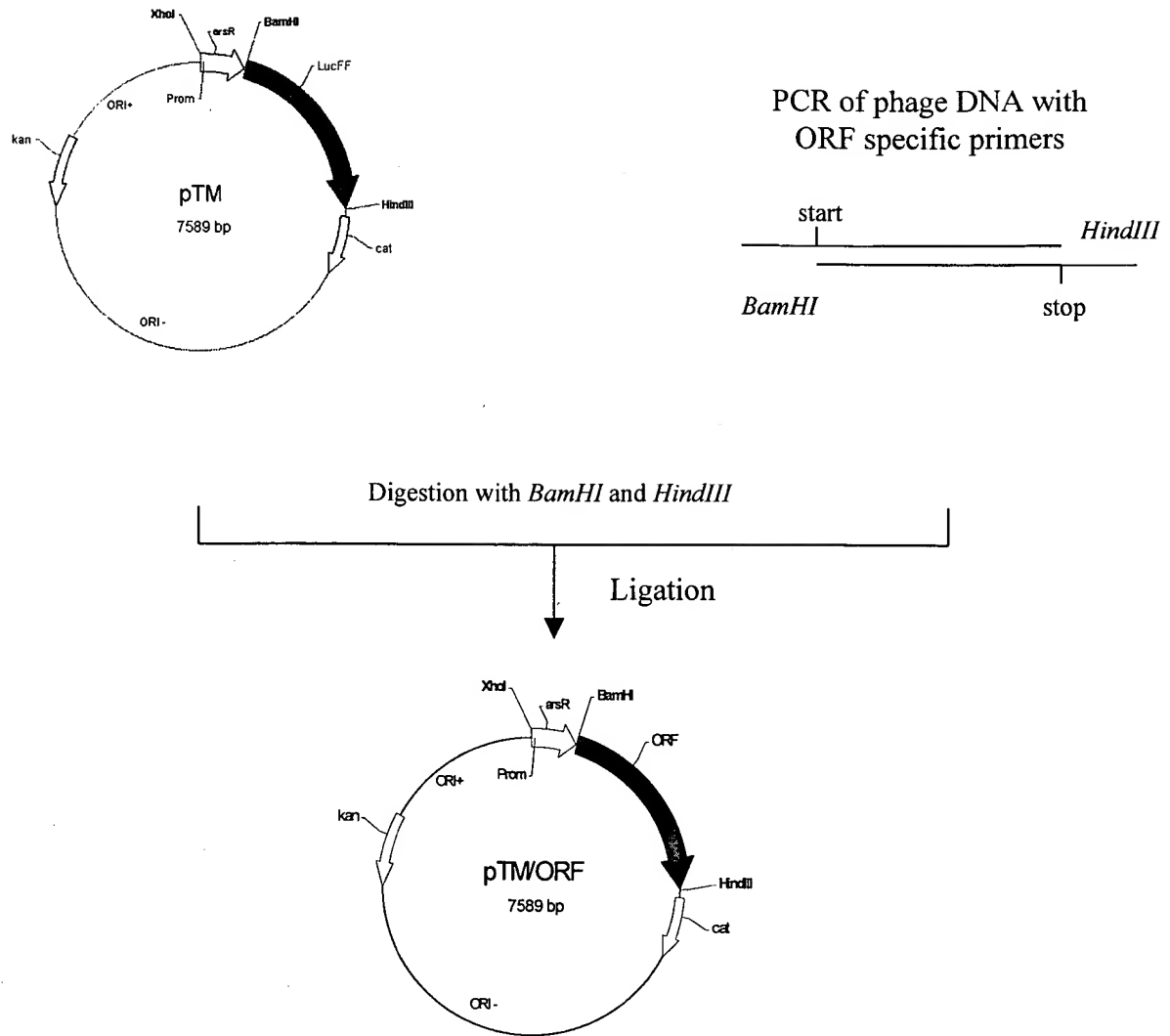
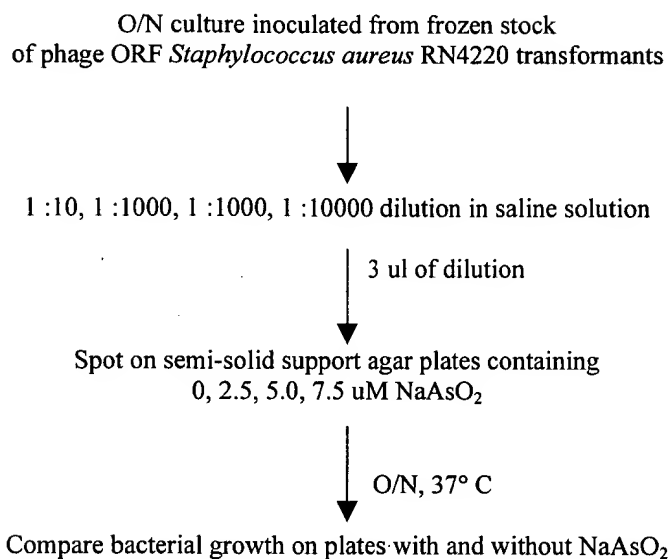


FIGURE 3

A) **Functional assay on semi-solid support medium**



B) **Functional assay in liquid medium**

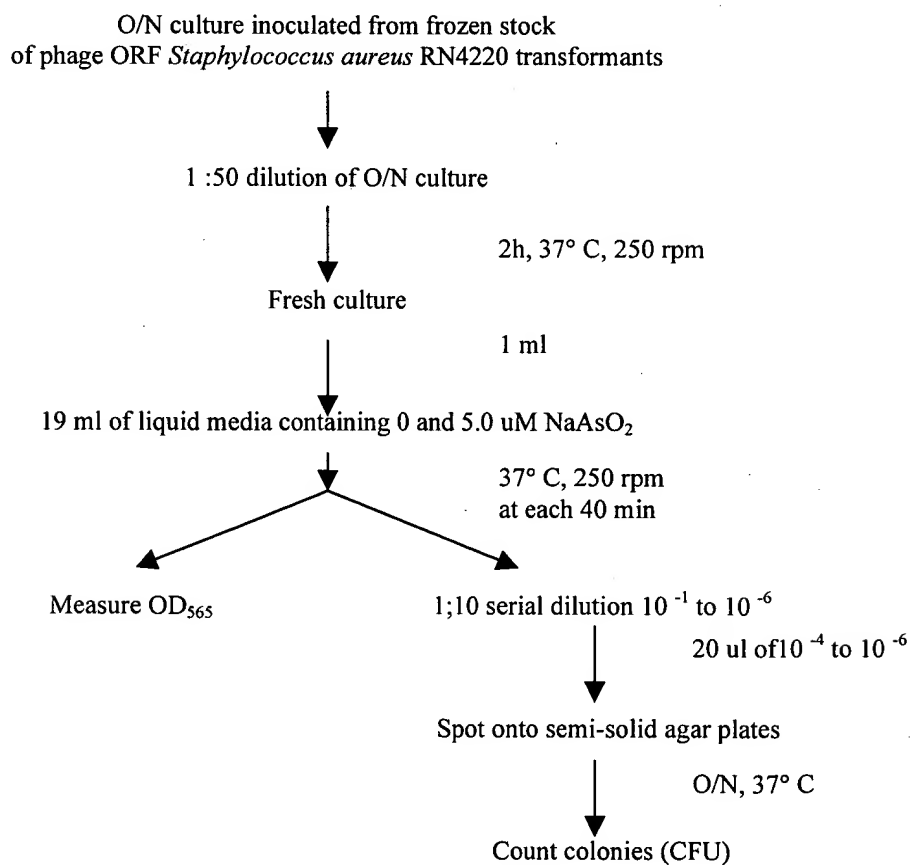


FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

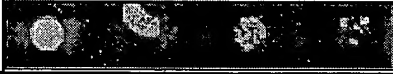

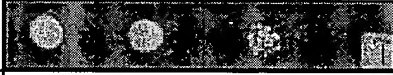
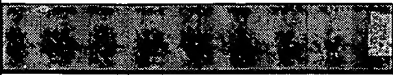

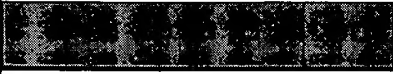







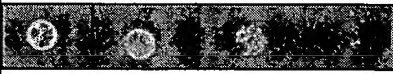
UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.



FIGURE 4B

B-

ORF ID	<i>Staphylococcus aureus</i> transformants	Semi-solid support media		
		Without induction		With induction (5 uM sodium arsenite)
44AHJDORF12	Clone1			
	Clone2			
	Clone3			
44AHJDORF25	Clone1			
	Clone2			
	Clone3			
Control 77ORF30	Clone1			

001001"000000

A-

FIGURE 5A

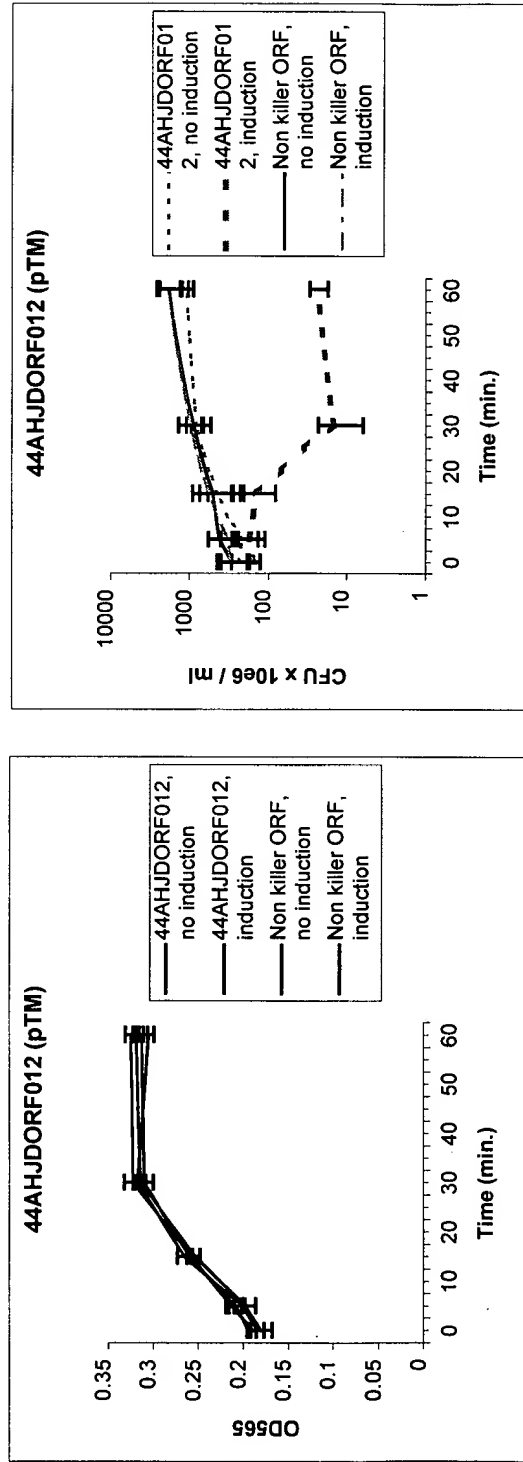
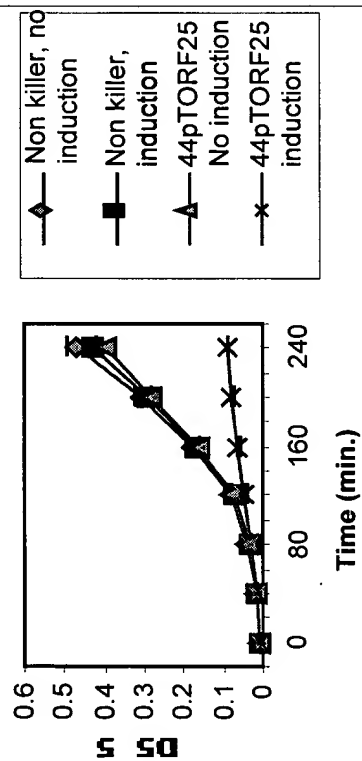
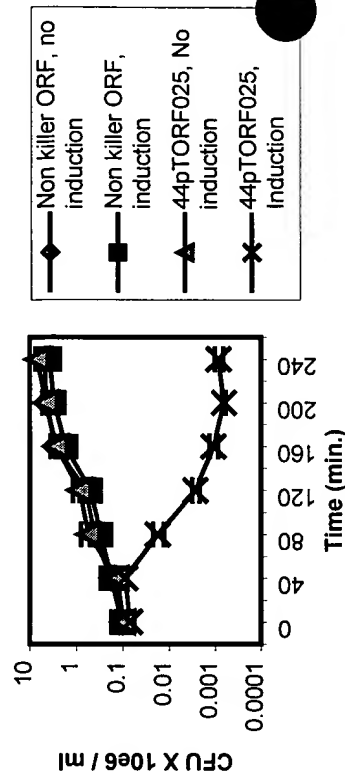


Fig  
.5B

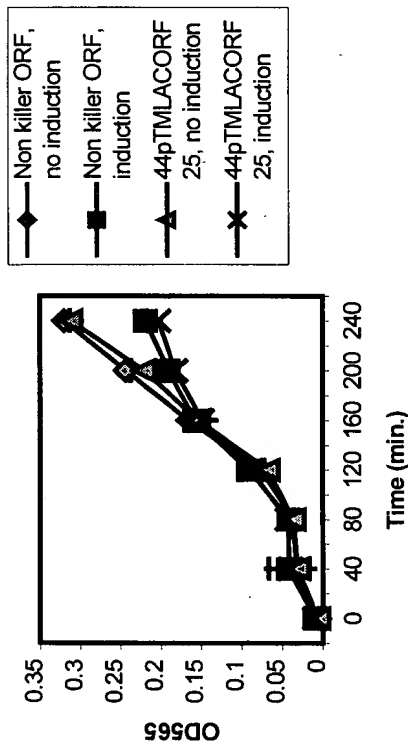
# 44AHJDORF025 (pT) 00T00T



# 44AHJDORF025 (pT)



# 44AHJD ORF 25 (pTMLac)



# 44AHJDORF25(pTMLac)

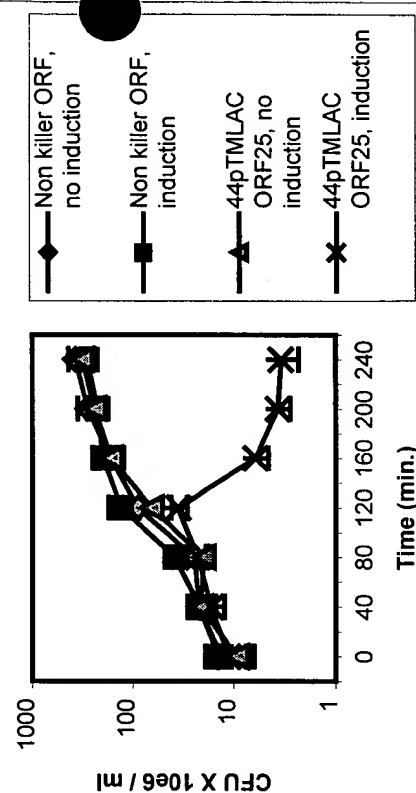
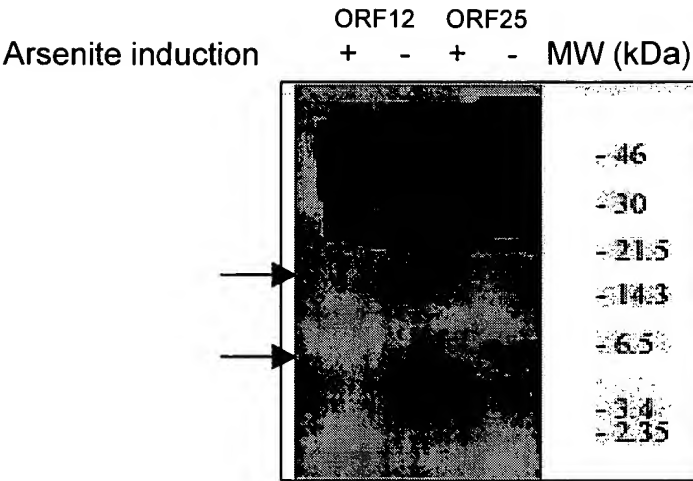


FIGURE 6



001021-2002000

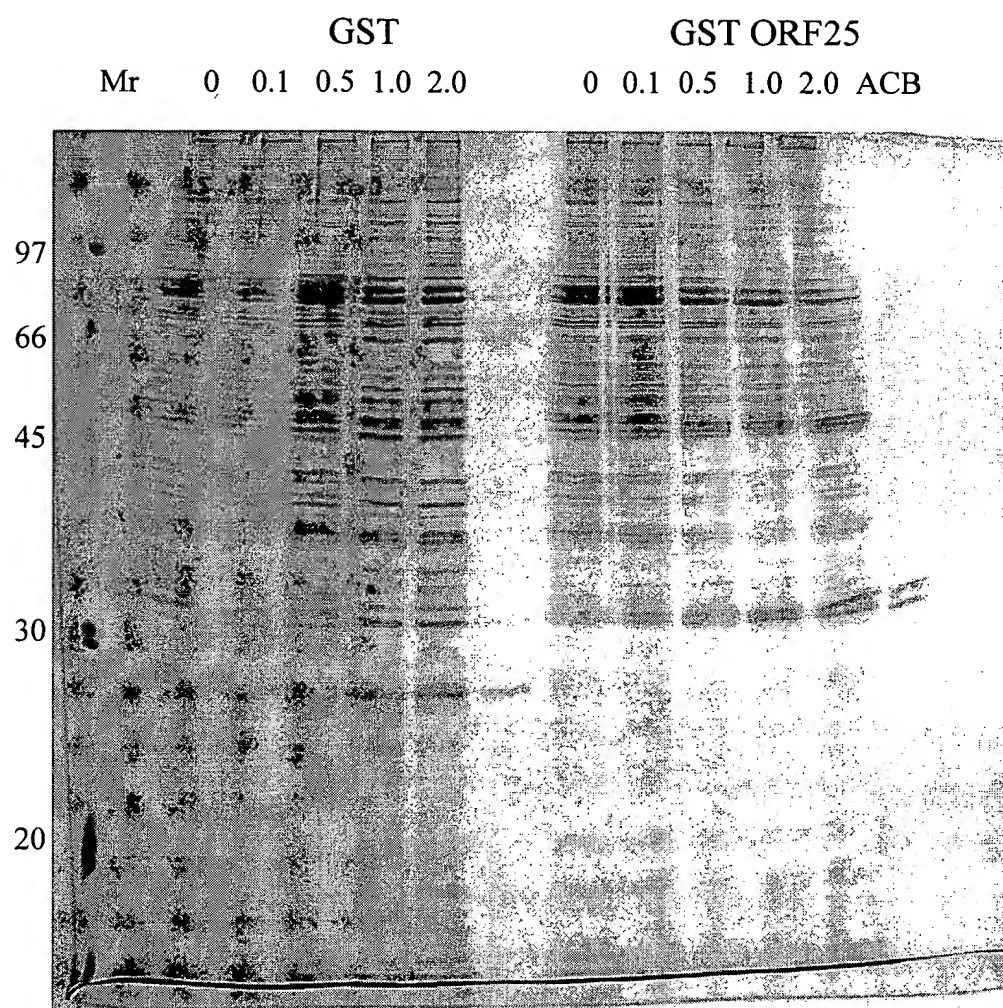
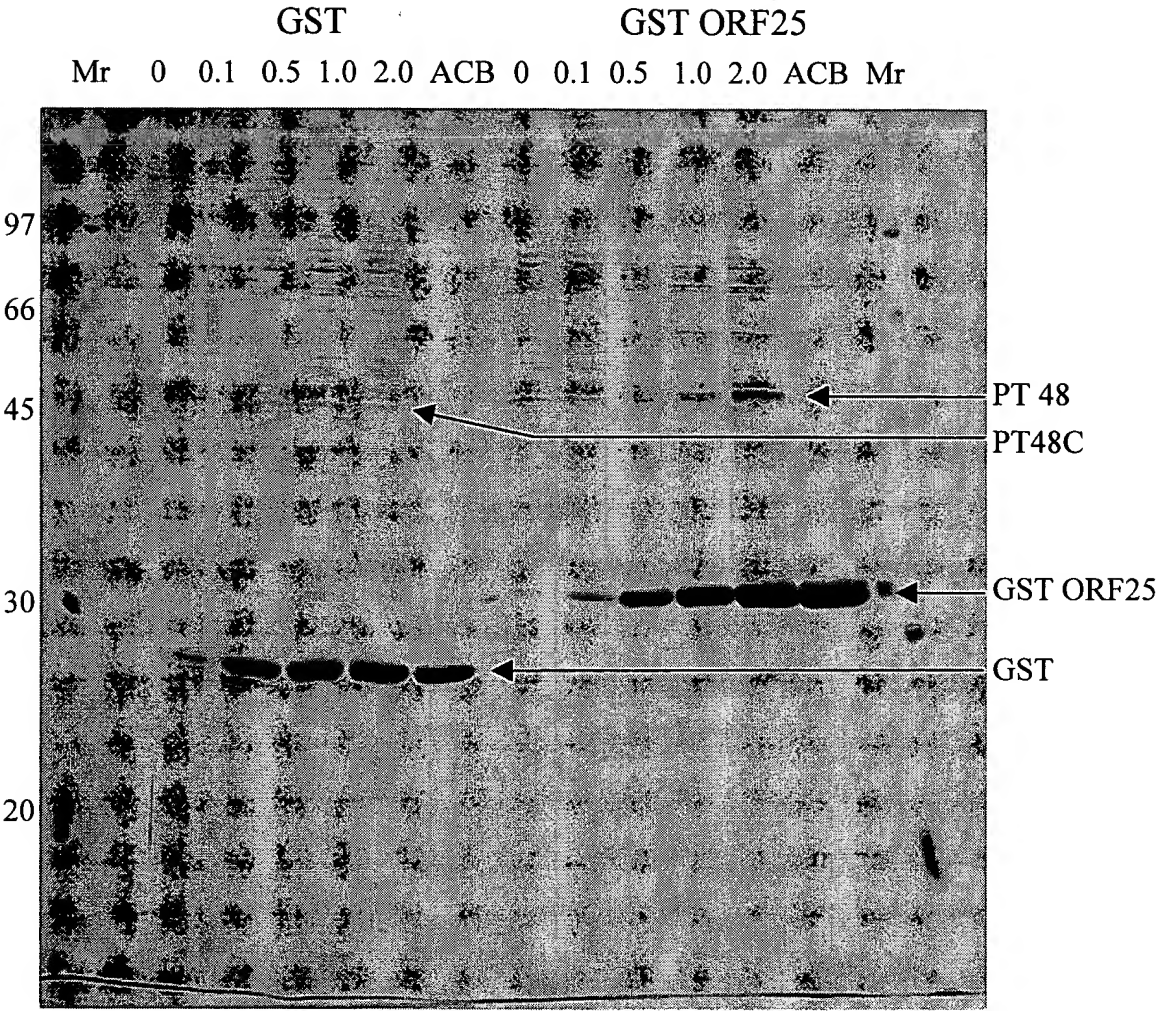
[illegible]

FIGURE 7B

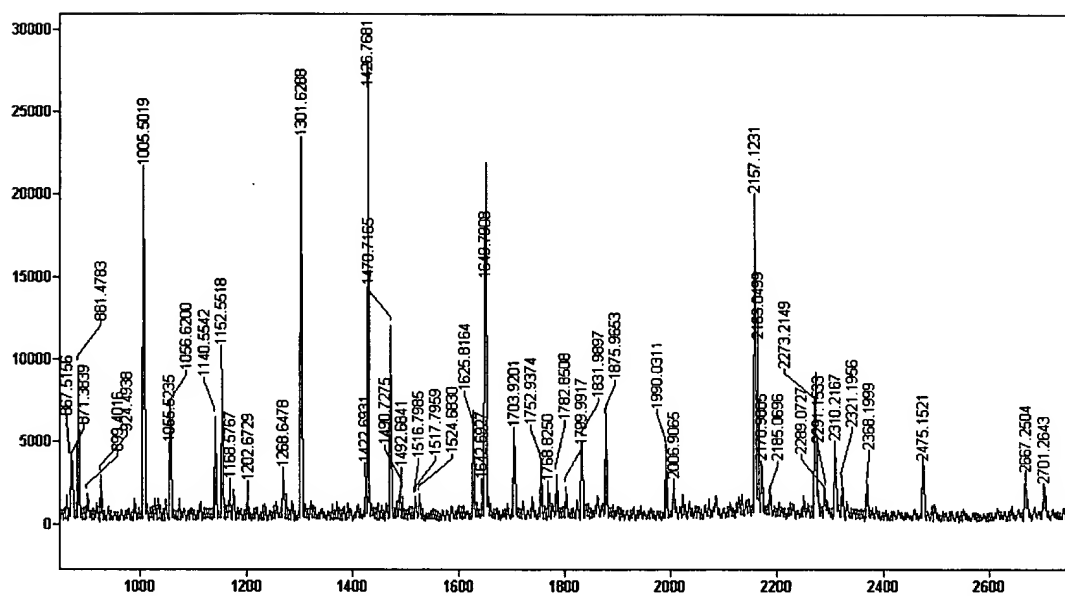


001021-268260

FIGURE 8

Tryptic peptide mass spectrum of 48 kDa interacting protein

(from Figure 1B)



# FIGURE 9

## Identification of PT48 as DNA-directed DNA polymerase III beta.

Details for: PT48

gi|1706496|sp|P50029|DP3B STAAU DNA POLYMERASE III BETA CHAIN

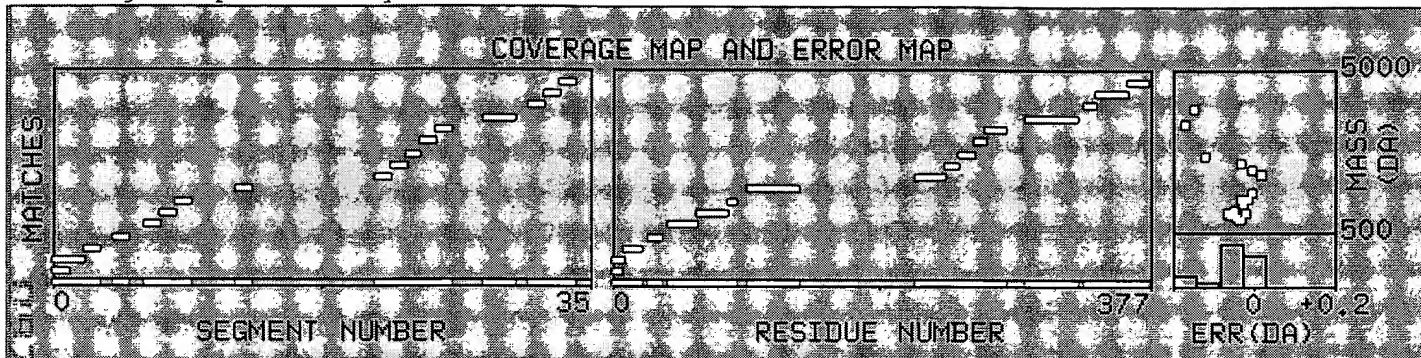
gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%



Measured Mass(M)	Avg/ Mono	Computed Mass	Error (Da)	Residues Start	To	Missed Cut	Peptide sequence
870.370	M	870.397	-0.027	333	339	0	YMDALK
880.474	M	880.505	-0.032	82	88	0	FFVDLIK
898.392	M	898.429	-0.037	1	7	0	MMEFTIK
1004.492	M	1004.540	-0.048	235	243	0	VGNVNFISR
1054.514	M	1054.530	-0.016	1	8	1	MMEFTIKR
1055.603	M	1055.658	-0.055	26	35	0	TTLPILTGK
1151.546	M	1151.586	-0.040	255	263	0	LFPENYEIK
1300.619	M	1300.641	-0.021	244	254	0	LLEGHYPDTR
1425.769	M	1425.782	-0.013	363	375	0	GDDSVTQLLPIR
1469.713	M	1469.740	-0.026	9	20	0	DYFITQLNDTLK
1648.781	M	1648.784	-0.003	264	277	0	LSTDNGEFYHADR
2156.112	M	2156.095	0.017	61	81	0	TVDGEDIVNISETGSVVLPR
2309.198	M	2309.199	-0.000	40	60	0	EHEVILTGSDSEISIEITPK
2474.139	M	2474.166	-0.027	214	234	0	IMSDNEEDIDIFFASNOVLEK
2666.266	M	2666.365	-0.099	340	362	0	AIDNDEVEVEFFGTMKPFLLKPK
3577.670	A	3577.809	-0.139	292	326	1	LSTGDDVVELSSTSPKIGTVKEEVDANDVEGGSIK
4033.298	A	4033.421	-0.123	97	132	0	LSTNEOFOTLITSGHSEFNLSGLDPDOYPLLPOVSR



## FIGURE 10

### SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCACTATTAAAGAGATTATTTTATTACACAATTAAATGACACATTAAAA  
GCTATTTACCAAGAACAACATTACCTATATTAAGTGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAAGTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATATTTAGAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCCAGACATTAATTACATCAGGTCATTCTGAATTTAATTTAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC  
CCAGTACTAACTGGTGTGAACTGGCTTATACAAGAAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAATAAAATTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTATTTAAAGTTGGAAATGTGAACTTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCCTGAAAACAT  
GAAATTAATTAAGTATAGACAATGGGGAGTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAAATTAAGTACAGGTGATGACGTTGTTGAA  
TTGCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT  
GAAGGTGGTAGCCTGAAAATTTCAATCACTCTAAATATATGATGGATGCTTTAAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCTTCGGTACAATGAAACCATTATTTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

### SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
*Staphylococcus aureus*

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGIKIDAKEHEVILTGSDSEISIEITIPKTVDGEDIVNI  
SETGSVVLPGRRFFVDIIKKLPKGDVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSV  
KVLKNVIAQTNFAVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNV IIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKVGNNVFISRLLEGHPDTRLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEVDANDVEGSLKISFNSKYMMDALKAIDNDEVEVEF  
FGTMKPFILKPKGDDSVTQLILPIRTY